AMENDMENTS TO THE SPECIFICATION

Please delete the title, page 1, line 3, and replace it with the following:

ACPL ANTIBODIES AND METHODS OF USE THEREOF

On page 1, after the title, please amend the section added by the Preliminary Amendment of February 6, 2004 as follows:

--CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation of U.S. Patent Application Serial No. 10/212,356, filed August 2, 2002, now U.S. Patent No. 6,692,740 ~~allowed~~, which is a divisional of U.S. Patent Application No. 09/616,530, filed on July 14, 2000, now U.S. Patent No. 6,664,077, which is a national stage application filed pursuant to 35 U.S.C. § 371 of international application PCT/US99/01420, filed on January 22, 1999, which claims the benefit under 35 U.S.C. § 119(e) of U.S. Provisional Application Serial No. 60/072,301, filed January 23, 1998, and U.S. Provisional Application Serial No. 60/078,835, filed March 20, 1998, all of which are incorporated by reference herein. –

On page 3, please amend the paragraph starting at line 9 as follows:

When a peptide fingerprint of an unknown protein is obtained, this can be compared to a database of known proteins to assist in the identification of the unknown protein (W.J. Henzel et al., *Proc. Natl. Acad. Sci. USA* 90:5011-5015, 1993; B. Thiede et al., *Electrophoresis 1996*, 17:588-599, 1996). A variety of computer software programs are accessible via the Internet to the skilled artisan for the facilitation of such comparisons, such as MultiIdent ~~(Internet site: www.expasy.ch/sprot/multiident.html)~~, PeptideSearch ~~(Internet site: www.mann.embl-heiedelberg.de...deSearch/FR_PeptideSearchForm.html)~~, and ProFound ~~(Internet site: www.chait-sgi.rockefeller.edu/cgi-bin/prot-id-frag.html)~~. These programs allow the user to specify the cleavage agent and the molecular weights of the fragmented peptides within a designated tolerance. The programs compare these molecular weights to protein databases to assist in the elucidation of the identity of the sample protein. Accurate information concerning the number of fragmented peptides and the precise molecular weight of those peptides is required for accurate identification. Therefore, increasing the accuracy in the determination of the number of fragmented peptides and the precise molecular weight of those peptides should result in enhanced success in the identification of unknown proteins.

On page

On page 15, please amend the paragraph starting at line 6 as follows:

Other derivatives include covalent or aggregative conjugates of the polypeptides with other proteins or polypeptides, such as by synthesis in recombinant culture as N-terminal or C-terminal fusions. Examples of fusion proteins are discussed below in connection with oligomers. Further, fusion proteins can comprise peptides added to facilitate purification and identification. Such peptides include, for example, poly-His or the antigenic identification peptides described in U.S. Patent No. 5,011,912 and in Hopp et al., *Bio/Technology* 6:1204, 1988. One such peptide is the FLAG® peptide, Asp-Tyr-Lys-Asp-Asp-Asp-Asp-Lys (SEQ ID NO:8), which is highly antigenic and provides an epitope reversibly bound by a specific monoclonal antibody, enabling rapid assay and facile purification of expressed recombinant protein. A murine hybridoma designated 4E11 produces a monoclonal antibody that binds the FLAG® peptide in the presence of certain divalent metal cations, as described in U.S. Patent 5,011,912, hereby incorporated by reference. The 4E11 hybridoma cell line has been deposited with the American Type Culture Collection under accession no. HB 9259. Monoclonal antibodies that bind the FLAG® peptide are available from Eastman Kodak Co., Scientific Imaging Systems Division, New Haven, Connecticut.

On page 32, please amend the paragraph starting on line 20 as follows:

For example, chromosomes can be mapped by radiation hybridization. First, PCR is performed using the Whitehead Institute/MIT Center for Genome Research Genebridge4 panel of 93 radiation hybrids ~~(http://www-genome.wi.mit.edu/ftp/distribution/human_STS_releases/july97/rhmap/genebridge4.html)~~. Primers are used which lie within a putative exon of the gene of interest and which amplify a product from human genomic DNA, but do not amplify hamster genomic DNA. The results of the PCRs are converted into a data vector that is submitted to the Whitehead/MIT Radiation Mapping site on the internet ~~(http://www-seq.wi.mit.edu)~~. The data is scored and the chromosomal assignment and placement relative to known Sequence Tag Site (STS) markers on the radiation hybrid map is provided. ~~The following web site provides additional information about radiation hybrid mapping: http://www-genome.wi.mit.edu/ftp/distribution/human_STS_releases/july97/07-97.INTRO.html).~~

On page 53, please amend the paragraph starting on line 22 as follows:

Identification of Unknown Proteins

As set forth above, a polypeptide or peptide fingerprint can be entered into or compared to a database of known proteins to assist in the identification of the unknown protein using mass spectrometry (W.J. Henzel et al., Proc. Natl. Acad. Sci. USA 90:5011-5015, 1993; D. Fenyo et al., Electrophoresis 19:998-1005, 1998). A variety of computer software programs to facilitate these comparisons are accessible via the Internet, such as Protein Prospector ~~(Internet site: prospector.ucsf.edu)~~, MultiIdent ~~(Internet site: www.expasy.ch/sprot/multiident.html)~~, PeptideSearch ~~(Internet site:www.mann.embl-heiedelberg.de...deSearch/FR_PeptideSearch Form.html)~~, and ProFound ~~(Internet site:www.chait-sgi.rockefeller.edu/cgi-bin/ prot-id-frag.html)~~. These programs allow the user to specify the cleavage agent and the molecular weights of the fragmented peptides within a designated tolerance. The programs compare observed molecular weights to predicted peptide molecular weights derived from sequence databases to assist in determining the identity of the unknown protein.

On page 54, please amend the paragraph starting on line 1 as follows:

In addition, a polypeptide or peptide digest can be sequenced using tandem mass spectrometry (MS/MS) and the resulting sequence searched against databases (J.K. Eng, et al., J. Am. Soc. Mass Spec. 5:976-989 (1994); M. Mann and M. Wilm, Anal. Chem. 66:4390-4399 (1994); J.A. Taylor and R.S. Johnson, Rapid Comm. Mass Spec.11:1067-1075 (1997)). Searching programs that can be used in this process exist on the Internet, such as Lutefisk 97 ~~(Internet site: www.lsbc.com:70/Lutefisk97.html)~~, and the Protein Prospector, Peptide Search and ProFound programs described above.